

a test agent, and (ii) ascertaining the presence, and more preferably the level, of onset or degree of severity of an inflammatory bowel disease or disorder, and comparing that with an untreated transgenic animal or transgenic animal treated with a control agent.

X. Exemplification

The following Table 1 teaches genes whose up
regulation or down-regulation, as indicated by "î" and "↓",

respectively, has been found to be associated with UC and

CD. The genes are grouped according to their general

functionality, as follows,

I Chemokines + cytokines and growth factors

15 II Inflammatory mediators

III Cell cycle regulators/ transcription factors

IV Cancer Related

V HLA or immune function genes

VI Antimicrobial

20 VII ECM and remodelling

VIII Others: Carbohydrate metabolism, Fatty acid

metabolism, Protein

folding/modification/degradation

25 Table 1

	σc		Acc No.	Gene Names	Chromosome	Microsatellite Markers
I	121.4	12.8	Y00787	MDNCF/IL-8	4q13-q21	D4S392-D4S2947
I	↑15.3	Ī	X54489	MGSA (GRO1)	4q21	D4S400-D4S1534
I	↑7.9		M57731	MIP-2 (GRO2)	4q21	D4S392-D4S2947
I	18.9	<u>↑4.1</u>	M28130	IL8	4q13-q21	D4S392-D4S2947
I	↑6.8	↑3.9	X57351	IP-10	11	pTEL-D11S1318
I	1 6		J04130	MIP-1 /SCYA4	17q21	D17S933-D17S800
I	↑3.4		X53800	MIP-2 (GRO3)	4q21	D4S400-D4S1534
I	13.2		M69203	MIP-1 /SCYA2	17q21	D17S933-D17S800

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		OC .	CD .	Acc No.	Gene Names	Chromosome	Microsatellite Markers
	I	14.6		X04500	pro-IL-1	2q14	D2S293-D2S121
	I	↑3.5		X53296	IL-1RA	2q14	D2S293-D2S121
	I	↑3.3		X04602	IL-6	7q21	D7S829-D7S673
	I	1 3		J03756	Growth hormone 2 (GH2)	17q22-q24	D17S794-D17S795
	I	↓ 3.5		D16431	Hepatoma-derived	17q2-q24	D17S794-D17S795
					growth factor (HDGF)		
	I		↓4	M58286	TNF Receptor member 1A	12p13.2	D12S99-D12S358
	II	↑35.5		S75256	Neutrophil lipocalin (HNL)	-	-
	II	110.4		X99133	Neutrophil	9q34	D9S1821-D9S159
					gelatinase-		
					associated lipocalin (NGAL)		
	II	↑8.7	<u> </u>	X85781	Nitric oxide	1	-
		<u> </u>			synthase (NOS2)		
	II	↑5.1		X65965	Mitochondrial	6q25.3	D6S442-D6S1581
					superoxide dismutase (SOD2)		
	II	1 5.5	14.5	M22430	Phospholipase A2,	1p35	
			, , , ,		group IIA	_	
		•			(PLA2G2A)		
		↑5.3		X51441	(SAA)	llp	-
		↑3.9		J03474	Serum amyloid A (SAA1)	11p15.1	D11S921-D11S1369
	II	↑3.7		M21119	Lysozyme	-	-
	II	↑3.4		D00408	Cytochrome P450 IIIA, polypeptide 7 (CPY3A7)	7	D7S479-D7S2545
	II	↓4.2		i	Anti-oxidant protein 2	1 .	D1S2790-D1S2640
	II	↓4.4			Metallothionein	-	-
	II	↓ 8		1	Metallothionein- 1G (MT1G)	16q13	D16S3057-D16S514
	II.	1 9			Nitric oxide synthase 2	10.	D10S1786-D10S541
	III	↑155	117.8		Regenerating	2p12	D2S286-D2S169
					islet-derived 1 (REG1B)		
	III	↑ 75	136.4	1		2p12	D2S139-D2S289
				-	islet-derived l (REG1A)		
	III	19.7	10.2			2p12	D2S169-D2S139
				i i	associated protein (PAP)	. !	
	III	↑58.8			Zinc Finger	-	_
İ				HT3769	Proteins		
	III	↑55.1	12.5				D14S65-qTEL
	III	↑17.5	↑4.7		S100A9/calgranuli n 3		D1S514-D1S2635
	III	10.8	↑3.6	: ;		11q23.1	D11S1347-D11S939
İ					methyltransferase		·
L					(NNMT)		,

			,		1=:	· · · · · · · · · · · · · · · · · · ·
	UC .	CD .	Acc No.	Gene Names	Chromosome	Microsatellite
	<u> </u>		ļ	<u> </u>	<u> </u>	Markers
V	↓4.2	↓3.4	M13755	Inteferon	1	D1S243-D1S468
				stimulated		
ł				protein 15-kDa		
				(ISG15)		
l v		↓3.4	D11086	IL-2 receptor	Xq13.1	DXS983-DXS995
				chain (IL2RG)		
v	↓ 3	↓ 6	M84526	Complement factor	-	pTEL-D19S413
				D (DF)	ļ	
V	↓ 3.9		M38690	CD9 antigen	12p13	D12S99-D12S358
v	<u> </u>		M28590	MHC Dg	6	
VI	1	1	M97925	Defensin 5	gnter-n21	D8S552-D8S549
"	120.4	140.8	1497925	(DEFA5)	opcer-pzi	
VI	16.8	↑ _{7.7}	U33317	Defensin 6	lanter-n21	D8S277-D8S550
\ \ \ \ \ \ \	16.8	17.7	033317	(DEFA6)	opeci pzi	503277 503330
VII	116.2	<u>.</u> ↑a -	L23808	MMP-12	11q22.2-	n1151339-
A T. T	116.2	13.3	000	(Macrophage		D11S1343
				elastase)	422.3	
VII	16.4		J05070	MMP-9 (Gelatinase	20011 2-	D20S119-D20S197
1 411	10.4		303070	B)	q13.1	
VII	114.7		X54925	MMP-1	11q22.3	D11S1339-
***	14./			(Interstitial	11422.3	D11S1343
				collagenase)		21201013
VII	14.2		X05232	MMP-3	11q22.3	D11S1339-
'	17.2			(Stromelysin 1)	<u></u>	D11S1343
VII	113 3	^	L10343	Elastase specific	20g12-g13	D20S119-D20S197
	113.3	13.6		inhibitor	- 1	
1				(Elafin)		
VII	11	↑3.1	Z74616	COL1A2	2q37	D2S2158-D2S125
VII	↑7.3		X52022	COL6A3	2q37	D2S2158-D2S125
VII	<u>:</u>	↑3.6	M55998	COL1A1	17q21.3-	D17S791-D17S794
	10.5	13.0			q22	
VII	14.8		X06700	COL3A1	2q31 .	D2S2257-D2S115
VII	↑4.7		X15882	COL6A2	21q22.3	_
	↑3.9	<u> </u>	X05610	t	1	D13S285-qTEL
			<u> </u>	1		D130203 Q1HD
VII.	↑3.7		HG2157-	Mucin 4 (MUC4)	3q29	-
	1		HT2227	manfoil forter ?	121~22 2	D0101070
ATI	13.1		X52003	Trefoil factor 1 (TFF1)	21q22.3	D21S1259-qTEL
777 7	-	Λ. -	M2340C	(TFF1) Intestinal mucin	<u> </u>	
VII			M22406		5-22 2	DEC426 DEC456
AII	16.4		J03040	Osteonectin	1 -	D5S436-D5S470
	A	<u> </u>	W1 70 10	(SPARC)	q32	D100010 D10000
VII	14	13.2	X17042	Proteoglycan 1	10q22.1	D10S210-D10S537
7777	Λ.,		D11400	(PRG1) Peripheral myelin	17p12-	D175904 D175700
VII	13.9		D11428		p11.2	D17S804-D17S799
				protein 22 (PMP22)	P11.2	
VII	11.	<u> </u>	X02761	Fibronectin 1	2q34	D2S137-D2S164
1 477	13.8		12/01	(FN1)	~47=	223137-223104
TOTT	! ↑3.7		M77349	Transforming	5q31	D5S393-D5S500
1 * + +	13./			growth factor		
İ	[beta-induced (TGF)		
				I)		
VTT	↑3.2		D13666	Osteoblast	13	D13S267-D13S1253
1	ا ۲۰۵۱		213000	specific factor 2		
				(OSF-2)		
VTT	13.1		M10321		12p13.3	D12S99-D12S358
1 4	1,2.7	İ	1	-Cir Hillenfand		

		uc .	CD .	Acc No.	Gene Names	Chromosome	Microsatellite Markers
			1		factor		****
	VII	↑3		L09190	Trichohyalin (THH)	1q21-q23	D1S439-D1S459
30	VII			D88422	Cystatin A (CSTA)	3q21	-
	VII		↑4.7	X58199	Adducin 2 (ADD2)	2p13-p14	-
	VII		↑3.7	M86933	Amelogenin (AMELY)	Yp11.2	-
	VII		↓3.2	D45370	Adipose specific collagen-like 2 (APM2)	10	D10S1786-D10S541
	VII		↓3.8	X73501	Cytokeratin 20	-	-
35	VII	↓ 4		U60061	Zygin 2	2	D2S367- D2S2230;D2S177- D2S119
	VII		↓ 3	AF006087	Actin-related complex	3	D3S3591-D3S1283
	VII		↓ 6	D87460	Paralemmin	19p13.3	pTEL-D19S413
	VIII	↑50.5		D28416 ·	Esterase D (ESD)	q14.2	D13S328-D13S168
		↑4.7		M15656	Aldolase B	q22.2	D15S202-D15S157
40	VIII		1.0.5	J04040	Glucagon (GCG)	,	D2S156-D2S376
	VIII		↓4.4	L31801	Monocarboxylate transporter 1 (MCT1)	1p13.2- p12	D1S418-D1S514
	VIII	↓ 3		D10523	Oxoglutarate dehydrogenase (OGDH)	7p14-p13	D7S521-D7S478
	VIII	↓4		M12963	Alcohol dehydrogenase la (ADH1)	4q21-q23	-
		↓4. 5		Y00339	Carbonic anhydrase II (CA2)		D8S275-D8S273
45		↓4.9		L10955	Carbonic anhydrase IV (CA4)	17q23	-
			↓3.1	L05144	Phophoenolpyruvat e carboxykinase 1, soluble (PCK1)	20q13.31	D20S183-D20S173
'ব	VIII	13		U07158	Syntaxin 4A (STX4A)		-
	VIII		13	L27706	Chaperonin subunit 6A (CCT6A)		D7S530-D7S509
	VIII	↓ 7	[↓] 3.1	J04093	UDP-glycosyl- transferase 1 (UGT1)		D2S2158-D2S125
50	VIII	↓3.2		U20499	Sulfotransferase family 1A (SULT1A3)	16p11.2	_
	VIII	↓ 3	•	M15182	-glucuronidase (GUSB)	7q21.11.	-
	VIII	↓ 4		U08854	UDP glucuronosyltrans ferase precursor (UGT2B15)	4g13	D4S1619-D4S392

	nc .	CD ·	Acc No.	Gene Names	Chromosome	Microsatellite Markers
VIII	[↓5		D87292	Thiosulfate	22	D22S277-D22S283
				sulfurtransferase (TST)		
VIII	13	4	M22324	Aminopeptidase N/CD13 (ANPEP)	15q25-q26	D15S202-D15S157
VIII	↓12	↓ 7	M22960	Protective	20q13.1	D20S119-D20S197
				protein for b-		
				galactosidase (PPGB)		
VIII	113.4		X90908	Fatty acid	5q23-q35	-
				binding protein 6 (FABP6)		
VIII	-	14.1	J02874	Fatty acid	8q21	-
				binding protein 4 (FABP4)		·
VIII	. ↓3	İ	M10050	Fatty acid	11p15.5	D11S1318-D11S90
				binding protein 1 (FABP1)		
VIII	↓ 3		L24774	Mitochondrial d3,	-	
	1	 	D16001	d2-CoA-isomerase		D. 0.0.1.1.
VIII	↓4		D16294	Mitochondrial 3- oxoacyl-CoA	18	D18S1118-D18S47
				thiolase (ACAA2)	,	
VIII	14		M77144	3 b-	1013.1	D1S418-D1S514.
	-			hydroxysteroid		
				dehydrogenase		
	ļ			(HSD3B2))		
VIII	↓ 5		D10511	Mitochondrial	-	-
				acetoacetyl-CoA		
VIII	1 7		Z80345	thiolase Acyl-Coenzyme A	12g22-	D12S366-D12S340
* * * *	* /		200345	dehydrogenase (ACADS)	qter	D123360-D123340
VIII	17	 	L11708	17 b-	16q24.1-	D16S515-D16S422
	1			hydroxysteroid	q24.2	
				dehydrogenase II		
	<u> </u>	<u> </u>		(HSD17B2)		
VIII	↓ 7		U26726	11 b-		D16S3031-
				hydroxysteroid		D16S3139
		1		dehydrogenase II (HSD11B2)		
VIII	↓3.5		X93036	MAT8 protein	19	D19S425-D19S418
	↓12.2	14	M97496	Guanylate cyclase	!	D1S2843-D1S417
	12.2	1		activator 1B		
				(UCA1B)		
VIII		↑4.2	D17400		10q22	D10S210-D10S537
				tetrahydropterin		
VIII		1 2 2	D21262	synthase (PCBD) KIAA0035		
VIII		,	AB002365		-	_
				<u> </u>	-	-
VIII		↓4.5	M11119	Endogenous retrovirus	-	-
			100000	envelope region		
/III	↓3.1		M19961	Mitochondrial	2cen-q13	D2S113-D2S176
			1	cytochrome c		
			1	oxidase Vb		